

09697006 092971

Figure 1

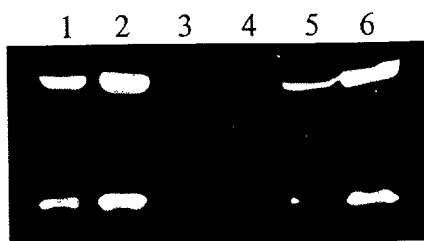


Figure 2

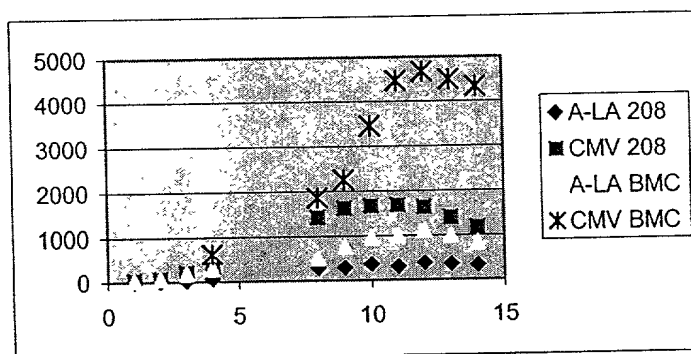


Figure 3

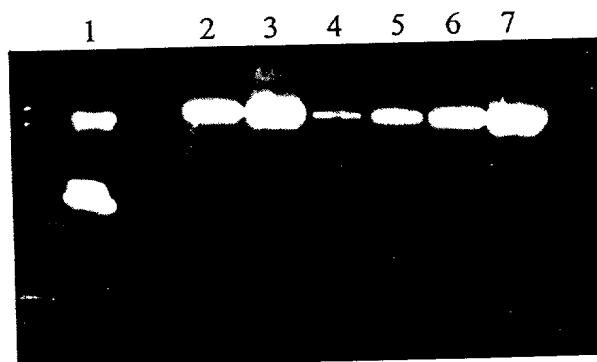


Figure 4  
SEQ ID NO:1

Hybrid Human-Bovine Alpha-Lactalbumin Promoter

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1      GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51     AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101    ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151    GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
201    AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251    GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAAATC
301    CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351    AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGGAAGTCTTA
401    AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451    AGAGACTGATGTAGAGAGAATGAGCCCTGGCATAACCAGAAGCTAACAGCT
501    ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
551    GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
601    CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCCAGAAT
651    CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701    GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTTCGATCCCTGG
751    CTTGGGAAGATCCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801    ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851    ATTGCAAAGAGTTGAACACAACCTGAGCAACTAAGCACAGCACAGTACAGT
900    ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCATGCAGGGTCTCCTGC
951    ATTGCAAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001   CTGGAGTGGGTAGCCTATTCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051   TTGAAGCTGGAGTCTCCTGCATTTTCAGGTGGATTCTTCACCAGCTGAACCTA
1101   CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTTCCCA
1151   CCTTTCCCAAAAAGGTTGGGTCACTCTTTTAAACCTTCTGTGGCCTACT
1201   CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251   GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301   GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351   ATACACACTTTTCAAGTTCTCCATTTTGTGAAATAGAAAGTCTCTGGAT
1401   CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451   TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501   TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551   TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601   TGACATACACCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651   AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701   ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751   CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801   GCAGGATCATGGTTTGAAGTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851   GACTAGATACTGGGAGAGGGAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901   AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951   CTCTTCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001   GAATATAAATATATGAACTGAGTGATGCTTCCATTTTCAGGTTCTTGGGG
2051   GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGAGGGGGGGCCCGGTAC
2101   C

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- 1 - 1525      Bovine alpha lactalbumin 5' flanking region (-2000 to -550 from the bovine alpha-lactalbumin transcription start point)
- 1526 - 2056      Human alpha-lactalbumin 5' flanking region (-600 to +15 from the human alpha-lactalbumin transcription start point)
- 2057 - 2101      Multiple cloning site

**Figure 5**  
**SEQ ID NO:2**  
**Mutated PPE Sequence**

```
1      GATTACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAACATCT
51     ACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGGACGCG
101    GCGGTGGTAATTACAAGCGAGGATCCGATTACTTACTGGCAGGTGCTGGG
151    GGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCTCGACC
201    AGGGTGAGATATCGGCCGGGGACGCGCGGTGGTAATTACAAGCG
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1 - 119      Mutated PPE
120 -126     Linker
127 - 245    Mutated PPE
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106290" 90026260

**Figure 6**  
**SEQ ID NO:3**  
**IRES-Signal Peptide Sequence**

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1   GGAATTGCCCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCG
51  CTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTCCACCATAT
101 TGCCGTCTTTTGGCAATGTGAGGGCCCGAAACCTGGCCCTGTCTTCTTG
151 ACGAGCATTCTAGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCT
201 GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAA
251 CAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCACCTGGCGAC
301 AGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATAACCTGCAAAGGC
351 GGCACAACCCCACTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCA
401 AATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAG
451 GTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC
501 ATGTGTTTAGTCGAGGTTAAAAAACGTCTAGGCCCCCGAACCACGGGG
551 ACGTGGTTTTCTTTGAAAAACACGATGATAATATGGCCTCCTTTGTCTC
601 TCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGGCGCCATGG
651 GATATCTAGATCTCGAGCTCGCGAAAGCTT

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1 - 583	IRES
584 - 640	Modified bovine alpha-lactalbumin signal peptide coding region
641 - 680	Multiple cloning site

F06290-9002660

**Figure 7a**  
**SEQ ID NO:4**  
**CMV MN14 Vector**

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1   CGGATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAA
51  TATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACA
101 TTTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTG
151 ACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATA
201 TATGGAGTTCGCGCTTACATAACTTACGGTAAATGGCCCGCTGGCTGAC
251 CGCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCAT
301 GTAACGCCAATAGGGACTTTCATTGACGTCAATGGGTGGAGTATTTACG
351 GTAAACTGCCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGC
401 CCCCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCCAG
451 TACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGT
501 CATCGCTATTACCATGGTGATGCGGTTTGGCAGTACATCAATGGGCGTG
551 GATAGCGGTTTGACTCACGGGGATTTCGAAGTCTCCACCCCATGACGTC
601 AATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCAAAATGTCTG
651 TAACAACCTCCGCCCCATTGACGCCAAATGGGCGGTAGGCATGTACGGTGGG
701 AGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGA
751 CGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAG
801 CCTCCGCGGGCCCCAAGCTTCTCGACGGATCCCCGGGAATTCAGGACCTCA
851 CCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGT
901 GTCCACTCCGAGGTCCAACCTGGTGAGAGCGGTGGAGGTGTTGTGCAACC
951 TGGCCGGTCCCTGCGCCTGTCTGCTCCGCATCTGGCTTCGATTTACCA
1001 CATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGG
1051 ATTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCT
1101 AAAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCC
1151 TGCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTTTGTGCA
1201 AGCCTTTACTTCGGCTTCCCCTGGTTTGCTTATTGGGGCCAAGGGACCCC
1251 GGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG
1301 CACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG
1351 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGC
1401 CCTGACCAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCTCAGGAC
1451 TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
1501 CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGA
1551 CAAGAGAGTTGAGCCCCAATCTTGTGACAAAACCTCACACATGCCACCGT
1601 GCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCTCTTCCCCCA
1651 AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGT
1701 GGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACG
1751 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG
1801 TACAACAGCACGTACCGTGTGGTCAGCGTCTCACCGTCTGCACCAGGA
1851 CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCC
1901 CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAA
1951 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
2001 GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCG
2051 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCT
2101 CCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGT
2151 GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
2201 ACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCC
2251 GGGAAATGAAAGCCGAATTCGCCCCCTCTCCCTCCCCCCCCCTAACGTTA
2301 CTGGCCGAAGCCGCTTGAATAAGGCCGGTGTGCGTTTGTCTATATGTTA
2351 TTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCCGAAACCTGG
2401 CCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTCCCCTCTCGCCAAAG
2451 GAATGCAAGGTCTGTTGAATGTCTGTGAAGGAAGCAGTTCTCTGGAAGCT
2501 TCTTGAAGACAAACAACGTCTGTAGCGACCCCTTGCAGGCAGCGGAACCC
2551 CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA
2601 CACCTGCAAAGGCGGCACAACCCAGTGCCACGTTGTGAGTTGGATAGTT
2651 GTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAA
2701 GGATGCCCCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGT
2751 GCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAACGTCTAGGCCCC
2801 CCGAACCACGGGGACGTGGTTTTCTCTTGAAAAACACGATGATAATATGG

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F05290-50025850

Figure 7b

2851 CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAG  
 2901 GCCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGG  
 2951 TGACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTG  
 3001 TAGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTAC  
 3051 TGGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTAGCGGTAGCGG  
 3101 TAGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACA  
 3151 TCGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTCGTTCCGGCCAA  
 3201 GGGACCAAGGTGGAAATCAAACGAACGTGTGGCTGCACCATCTGTCTTCAT  
 3251 CTTCCCGCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGT  
 3301 GCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTG  
 3351 GATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGA  
 3401 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAG  
 3451 CAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGC  
 3501 CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTAGAGATC  
 3551 TAGGCCTCCTAGGTGACATCGATAAAAATAAAAGATTTTATTTAGTCTCC  
 3601 AGAAAAAGGGGGGAATGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCT  
 3651 TAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGA  
 3701 GAAGTTCAGATCAAGGTGAGGAACAGATGGAACAGCTGAATATGGGCCAA  
 3751 ACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACA  
 3801 GATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTC  
 3851 CTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCC  
 3901 CTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGAC  
 3951 CTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCG  
 4001 CTTCTGTTGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCAAC  
 4051 CCTCACTCGGGGCGCCAGTCTCCGATTGACTGAGTCGCCCCGGGTACCC  
 4101 GTGTATCCAATAAACCTCTTGACAGTTGCATCCGACTTGTGGTCTCGCTG  
 4151 TTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTGAGCGGGGGTC  
 4201 TTTCATT

- 1 - 812 CMV promoter/enhancer
- 853-855 MN14 antibody heavy chain gene signal peptide start codon
- 2257 - 2259 MN14 antibody heavy chain gene start codon
- 2271 - 2846 EMCV IRES
- 2847 - 2849 Bovine alpha-lactalbumin signal peptide start codon
- 2904 - 2906 First codon mature MN14 antibody light chain gene
- 3543 - 3544 MN14 antibody light chain gene stop codon
- 3614 - 4207 MoMuLV 3' LTR

**Figure 8a**  
**SEQ ID NO:5**  
**CMV LL2 Vector**

1 GGATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAAT  
51 ATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACAT  
101 TTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTGA  
151 CTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATAT  
201 ATGGAGTTCGCGGTTACATAACTTACGGTAAATGGCCCGCTGGCTGACC  
251 GCCCAACGACCCCGCCCATGACGTCAATAATGACGTATGTTCCCATAG  
301 TAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTACGG  
351 TAAACTGCCCCTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCC  
401 CCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCCAGT  
451 ACATGACCTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAGTC  
501 ATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGG  
551 ATAGCGGTTTGACTCACGGGGATTTCGAAGTCTCCACCCCATGACGTCA  
601 ATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGT  
651 AACAACTCCGCCCCATTGACGCAAAATGGGCGGTAGGCATGTACGGTGGGA  
701 GGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGAC  
751 GCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGC  
801 CTCCGCGGCCCCAAGCTTCTCGACGGATCCCCGGGAATTTCAGGACCTCAC  
851 CATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTG  
901 TCCACTCCCAGGTCCAGCTGGTCCAATCAGGGGCTGAAGTCAAGAAACCT  
951 GGGTCATCAGTGAAGGTCTCCTGCAAGGCTTCTGGCTACACCTTTACTAG  
1001 CTACTGGCTGCACTGGGTGAGGACCTGGACAGGGTCTGGAATGGA  
1051 TTGGATACATTAATCCTAGGAATGATTATACTGAGTACAATCAGAACTTC  
1101 AAGGACAAGGCCACAATAACTGCAGACGAATCCACCAATACAGCCTACAT  
1151 GGAGCTGAGCAGCCTGAGGTCTGAGGACACGGCATTTTATTTTTGTGCAA  
1201 GAAGGGATATTACTACGTTCTACTGGGGCCAAGGCACCACGGTCACCGTC  
1251 TCCTCAGCCTCCACCAAGGGCCCCATCGGTCTTCCCCCTGGCACCCCTCCTC  
1301 CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT  
1351 ACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGCCCTGACCAGC  
1401 GCGGTGCACACCTTCCCGGTGTCTTACAGTCTCAGGACTCTACTCCCT  
1451 CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACA  
1501 TCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTT  
1551 GAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCAGCACC  
1601 TGAACCTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGG  
1651 ACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGAC  
1701 GTGAGCCACGAAGACCCTGAGGTCAAGTCAACTGGTACGTGGACGGCGT  
1751 GGAGGTGCATAATGCCAAGACAAGCCGCGGGAGGAGCAGTACAACAGCA  
1801 CGTACCGTGTGGTCAGCGTCTTACCGTCTTGCACCAGGACTGGCTGAAT  
1851 GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCCAGCCCCAT  
1901 GCAGAAAACCATCTCCAAGGCCAAAGGGCAGCCCCGAGAACCACAGGTGT  
1951 ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTG  
2001 ACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGA  
2051 GAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGTCTGG  
2101 ACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGC  
2151 AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCT  
2201 GCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGGAATGAA  
2251 AGCCGAATTGCCCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAG  
2301 CCGCTTGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCA  
2351 TATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTC  
2401 TTGACGAGCATTCTAGGGGTCTTCCCCCTCTCGCCAAAGGAATGCAAGG  
2451 TCTGTTGAATGTGCTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGAC  
2501 AAACAACGTCTGTAGCGACCCCTTTCAGGGCAGCGGAACCCCCACCTGGC  
2551 GACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAA  
2601 GGCGGCACAACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAG  
2651 TCAAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAG  
2701 AAGGTACCCCATTTGATGGGATCTGATCTGGGGCCTCGGTGCACATGCTT  
2751 TACATGTGTTTAGTCGAGGTTAAAAAACGTCTAGGCCCCCCGAACACG  
2801 GGGACGTGGTTTTCTTTGAAAAACACGATGATAATATGGCCTCCTTTGT

T06290-50045860

Figure 8b

2851 CTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGACATCC  
 2901 AGCTGACCCAGTCTCCATCATCTCTGAGCGCATCTGTTGGAGATAGGGTC  
 2951 ACTATGAGCTGTAAGTCCAGTCAAAGTGTTTATACAGTGCAAATCACAA  
 3001 GAACTACTTGGCCTGGTACCAGCAGAAACCAGGGAAAAGCACCTAAACTGC  
 3051 TGATCTACTGGGCATCCACTAGGGAATCTGGTGTCCCTTCGCGATTCTCT  
 3101 GGCAGCGGATCTGGGACAGATTTTACTTTCACCATCAGCTCTCTTCAACC  
 3151 AGAAGACATTGCAACATATTATTGTCACCAATACCTCTCCTCGTGGACGT  
 3201 TCGGTGGAGGGACCAAGGTGCAGATCAAACGAACTGTGGCTGCACCATCT  
 3251 GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTC  
 3301 TGTGTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT  
 3351 GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCA  
 3401 GAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCT  
 3451 GAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTACCCC  
 3501 ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT  
 3551 TAGAGATCTAGGCCTCCTAGGTCGACATCGATAAAAATAAAAGATTTTATT  
 3601 TAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCACCTGTAGGTTTGGCA  
 3651 AGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTG  
 3701 AGAATAGAGAAGTTTCAAGTCAAGGTGAGAACAGATGGAACAGCTGAATA  
 3751 TGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTGCCCGGGCTCAGGGC  
 3801 CAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTA  
 3851 AGCAGTTTCTGCCCGGGCTCAGGGCCAAGAACAGATGGTCCCAGATGCG  
 3901 GTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCC  
 3951 CCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTC  
 4001 GCTTCTCGCTTCTGTTTCGCGCGCTTCTGCTCCCGAGCTCAATAAAAGAG  
 4051 CCCACAACCCCTCACTCGGGGCGCCAGTCCCTCCGATTGACTGAGTCGCCC  
 4101 GGGTACCCGTGTATCCAATAAACCCCTCTGCAGTTGCATCCGACTTGTGG  
 4151 TCTCGCTGTTTCCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTGAG  
 4201 GTCTTTCATT

1 - 812 CMV promoter/enhancer  
 852 - 854 LL2 antibody heavy chain signal peptide start codon  
 2247 - 2249 LL2 antibody heavy chain stop codon  
 2261 - 2836 EMCV IRES  
 2837 - 2839 Bovine alpha-lactalbumin signal peptide start codon  
 2894-2896 First codon of mature LL2 antibody light chain gene  
 3551 - 3553 LL2 antibody light chain gene stop codon  
 3622 - 4210 MoMuLV 3' LTR

095900-9004550



**Figure 9a**  
**SEQ ID NO:6**  
**MMTV MN14 Vector**

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1      CGAGCTTGGCAGAAATGGTTGAACTCCCGAGAGTGTCTACACCTAGGGG
51     AGAAGCAGCCAAGGGGTGTGTTCCACCAAGGACGACCCGTCTGCGCACA
101    AACGGATGAGCCCATCAGACAAAGACATATTCACTCTGCTGCAAACCTT
151    GGCATAGCTCTGCTTTGCCTGGGGCTATTGGGGGAAGTTGCGGTTTCGTGC
201    TCGCAGGGCTCTCACCCTTGACTCTTTCAATAATAACTCTTCTGTGCAAG
251    ATTACAATCTAAACAATTTCGGAGAACTCGACCTTCCTCCTGAGGCAAGGA
301    CCACAGCCAACCTTCCTCTTACAAGCCGCATCGATTTTGTCTTCAGAAAT
351    AGAAATAAGAATGCTTGCTAAAAATTATATTTTACCAATAAGACCAATC
401    CAATAGGTAGATTATTAGTTACTATGTTAAGAAATGAATCATTATCTTTT
451    AGTACTATTTTTACTCAAATTCAGAAGTTAGAAATGGGAATAGAAAATAG
501    AAAGAGACGCTCAACCTCAATTGAAGAACAGGTGCAAGGACTATTGACCA
551    CAGGCCTAGAAGTAAAAAAGGGAAAAAGAGTGTTTTTGTCAAATAGGA
601    GACAGGTGGTGGCAACCAGGGACTTATAGGGGACCTTACATCTACAGACC
651    AACAGATTGCCCCCTTACCATATACAGGAAGATATGACTTAAATTGGGATA
701    GGTGGGTTACAGTCAATGGCTATAAAGTGTTATATAGATCCCTCCCCTTT
751    CGTGAAAGACTCGCCAGAGCTAGACCTCCTTGGTGTATGTTGTCTCAAGA
801    AAAGAAAGACGACATGAAACAACAGGTACATGATTATATTTATCTAGGAA
851    CAGGAATGCACTTTTGGGGAAAGATTTTCCATACCAAGGAGGGGACAGTG
901    GCTGGACTAATAGAACATTATTCTGCAAAAACTTATGGCATGAGTTATTA
951    TGATTAGCCTTGATTTGCCCAACCTTGCGGTTCCCAAGGCTTAAGTAAGT
1001   TTTTGGTTACAAACTGTTCTTAAAAACAAGGATGTGAGACAAGTGGTTTCC
1051   TGACTTGGTTTGGTATCAAAGGTTCTGATCTGAGCTCTGAGTGTTCTATT
1101   TTCCTATGTTCTTTTGGAAATTTATCCAAATCTTATGTAAATGCTTATGTA
1151   AACCAAGATATAAAGAGTGCTGATTTTTTGAGTAAACTTGCAACAGTCC
1201   TAACATTACCTCTTGTGTGTTTGTGTCTGTTCCGCATCCCGTCTCCGCT
1251   CGTCACTTATCCTTCACTTTCCAGAGGTCCTCCCGCAGACCCCGGCGAC
1301   CCTCAGGTCCGCGCACTGCGGCAGCTGGCGCGCGAACAGGGACCCCTCGGA
1351   TAAGTGACCCTTGTCTTTATTTCTACTATTTTGTGTTCTGTTCTGTTTGT
1401   CTCTATCTTGTCTGGCTATCATCACAAGAGCGGAACGGACTCACCTCAGG
1451   GAACCAAGCTAGCCCCGGGGTCGACGGATCCGATTACTTACTGGCAGGTGC
1501   TGGGGGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCTC
1551   GACCAGGGTGAGATATCGGCCGGGGACGCGCGGTTGGTAATTACAAGCGA
1601   GATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAA
1651   CATCTACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGG
1701   ACGCGCGCGGTGGTAATTACAAGCGAGATCCCCGGGAATTACAGGACCTCAC
1751   CATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTG
1801   TCCACTCCGAGGTCCAACCTGGTGGAGAGCGGTGGAGGTGTTGTGCAACCT
1851   GGCCGGTCCCTGCGCCTGCTCCTGCTCCGCATCTGGCTTCGATTTACCCAC
1901   ATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGGA
1951   TTGGAGAAATTCATCCAGATAGCAGTACGATTAAGTATGCGCCGTCTCTA
2001   AAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCTCT
2051   GCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTTGTGCAA
2101   GCCTTTACTTCGGCTTCCCCTGGTTTGCTTATTGGGGCCAAGGGACCCCG
2151   GTCACCGTCTCCTCAGCCTCCACCAAGGGGCCATCGGTCTTCCCCCTGGC
2201   ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGG
2251   TCAAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGCC
2301   CTGACCAGCGCGCTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACT
2351   CTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC
2401   AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC
2451   AAGAGAGTTGAGCCCCAATCTTGTGACAAAACCTCACACATGCCACCGTG
2501   CCCAGCACCTGAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCCTAA
2551   AACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG
2601   GTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGT
2651   GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGT
2701   ACAACAGCACGTACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAGGAC
2751   TGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCC
2801   AGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAAC

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T06290-90026850

09697006 062904  
T06290 90026860

Figure 9b

2851 CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAG  
2901 GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT  
2951 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTC  
3001 CCGTGCTGGACTCCGACGGCTCCTTCTTCCCTCTATAGCAAGCTCACCGTG  
3051 GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCA  
3101 CGAGGCTCTGCACAACCCTACACGCAGAAGAGCCTCTCCCTGTCTCCCG  
3151 GGAAATGAAAGCCGAATTCGCCCCCTCTCCCTCCCCCCCCCTAACGTTAC  
3201 TGGCCGAAGCCGCTTGAATAAGGCCGGTGTGCGTTTGTCTATATGTTAT  
3251 TTTCCACCATAATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGC  
3301 CCTGTCTTCTTGACGAGCATTCTAGGGGTCTTTCCCTCTCGCCAAAGG  
3351 AATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTT  
3401 CTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCC  
3451 CCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATAC  
3501 ACCTGCAAAGGCGGCACAACCCCAAGTCCACGTTGTGAGTTGGATAGTTG  
3551 TGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAG  
3601 GATGCCCAGAAGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTG  
3651 CACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAACGTCTAGGCCCCC  
3701 CGAACCACGGGGACGTGGTTTTCTTTGAAAAACACGATGATAATATGGC  
3751 CTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGG  
3801 CCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGGT  
3851 GACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTGT  
3901 AGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTACT  
3951 GGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTGAGCGGTAGCGGT  
4001 AGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACAT  
4051 CGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTGCTTCGGCCAAG  
4101 GGACCAAGGTGGAATCAAACGAACTGTGGCTGCACCATCTGTCTTCATC  
4151 TTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTG  
4201 CCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGAAGGTGG  
4251 ATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGAC  
4301 AGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGC  
4351 AGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCC  
4401 TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTAGAGATCC  
4451 CCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATAATCAACCTCTGGA  
4501 TTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACATGTTGCTCCTT  
4551 TTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCT  
4601 TCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTC  
4651 TCTTTATGAGGAGTTGTGGCCCCGTGTGTCAGGCAACGTGGCGTGGTGTGCA  
4701 CTGTGTTTGTGTCAGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGT  
4751 CAGTCTCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGA  
4801 ACTCATCGCCGCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGG  
4851 GCACTGACAATTCGTTGGTGTGTCGGGGAAATCATGTCCTTTCTTGG  
4901 CTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTA  
4951 CGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGC  
5001 CGGCTCTGCGGCCTCTTCCGCGTCTTCGCTTCGCCCTCAGACGAGTCGG  
5051 ATCTCCCTTTGGGCCGCTCCCGCCTGATCGATAACCGTCAACATCGATA  
5101 AAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCC  
5151 CACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCAT  
5201 GGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTGAGGAACA  
5251 GATGGAACAGCTGAATATGGGCCAAAACAGGATATCTGTGGTAAGCAGTTC  
5301 CTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAA  
5351 ACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACA  
5401 GATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCA  
5451 GATGTTTCCAGGGTCCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTG  
5501 AACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCTGCTCCC  
5551 CGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGGGCGCCAGTCTCTCC  
5601 GATTGACTGAGTCGCCCCGGTACCCGTGTATCCAATAAACCCCTCTTGCA  
5651 TTGCATCCGACTTGTGGTCTCGCTGTTTCTTGGGAGGGTCTCCTCTGAGT  
5701 GATTGACTACCCGTCAGCGGGGTCTTTTCATT

1 - 1457      Mouse mammary tumor virus LTR  
1475 - 1726      Double mutated PPE sequence

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**Figure 9c**

1752 - 1754	MN14 heavy chain signal peptide start codon
3156 - 3158	MN14 heavy chain stop codon
3170 - 3745	EMCV IRES
3746 - 3748	Bovine alpha-lactalbumin signal peptide start codon
3803 - 3805	First codon of mature MN14 light chain gene
4442 - 4444	MN14 antibody light chain gene stop codon
4487 - 5078	WPRE sequence
5133 - 5372	MoMuLV 3' LTR

105250" 300/15250

**Figure 10a**  
**SEQ ID NO:7**  
**Alpha-Lactalbumin MN14 Vector**

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1    AAAGACCCCAACCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCA
51   AGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTTCAAGGTCA
101  GGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGGTT
151  CCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATGGGCC
201  AAACAGGATATCTGTGGTAAGCAGTTCCCTGCCCCGGCTCGGGGCCAAGAA
251  CAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATCAT
301  CAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACCTTAT
351  TTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCCGCT
401  CTCCGAGCTCAATAAAAAGAGCCCAACCCCTCACTCGGCGCGCCAGTCT
451  TCCGATAGACTGCGTCGCCCCGGGTACCCGTATTCCCAATAAAGCCTCTTG
501  CTGTTTGCATCCGAATCGTGGTCTCGCTGTTTCTTGGGAGGGTCTCCTCT
551  GAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGTCCGG
601  GATTTGGAGACCCCTGCCAGGGACCAACCGACCCACCGGGAGGTAAG
651  CTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTG
701  ATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAAGCTCTGTATCTGG
751  CGGACCCGTGGTGGAAGTACGAGTTCTGAACACCCGGCCGCAACCCTGG
801  GAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGAGGAA
851  GGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGTAGGA
901  GACGAGAACCTAAAACAGTTCGCCCTCCGTCTGAATTTTGTCTTCCGGT
951  TTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTC
1001 TGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGC
1051 CAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAGATGT
1101 CGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGG
1151 TTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGCGA
1201 GACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTT
1251 TTCACCTGGCCCGCATGGACACCCAGACAGGTCCCCTACATCGTGACCT
1301 GGGAAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACAC
1351 CCTAAGCCTCCGCCTCCTCTTCTCCATCCGCCCCGTCTCTCCCCCTTGA
1401 ACCTCCTCGTTGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTC
1451 CTTCTCTAGGCGCCGGAATTCGATCTGATCAAGAGACAGGATGAGGATC
1501 GTTTCGCATGATTGAACAAGATGGATTGCACGACAGTTCTCCGGCCGCTT
1551 GGGTGGAGAGGCTATTCCGGCTATGACTGGGCACAACAGACAATCGGCTGC
1601 TCTGATGCCGCCGTGTTCCGGCTGTGACGCGAGGGGCGCCCGGTTCTTTT
1651 TGTCAAGACCGACCTGTCCGGTGCCTGAATGAACTGCAGGACGAGGCAG
1701 CGCGGCTATCGTGGCTGGCCACGACGGCGGTTCCCTGCGCAGCTGTGCTC
1751 GACGTTGTCACTGAAGCGGGAAGGACTGGCTGCTATTGGGCGAAGTGCC
1801 GGGGACAGGATCTCTGTCTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCA
1851 TCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGC
1901 CCATTGACACCAAGCGAAACATCGCATCGAGCGAGCACGTAATCGGAT
1951 GGAAGCCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGC
2001 TCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGC
2051 GAGGATCTCGTCTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGT
2101 GGAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGG
2151 CGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAG
2201 CTTGGCGGCGAATGGGCTGACCGCTTCTCGTGCTTTACGGTATCGCCGC
2251 TCCCGATTTCGACGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCT
2301 GAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGC
2351 CATCACGAGATTTGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTC
2401 GGAATCGTTTTCCGGGACGCGCGGCTGGATGATCCTCCAGCGCGGGGATCT
2451 CATGCTGGAGTTCTTCCGCCACCCCGGGCTCGATCCCTCGCGAGTTGGT
2501 TCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGC
2551 AAATCCGTCGGCATCCAGGAAACCAGCAGCGGCTATCCGCGCATCCATGC
2601 CCCGAACTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAGGCGG
2651 ATCCTAGAACTAGCGAAAATGCAAGAGCAAAGACGAAAACATGCCACACA
2701 TGAGGAATACCGATTCTCTCATTAACATATTACGCCAGTTATCTGGGCT
2751 TAAAAGCAGAAGTCCAACCCAGATAACGATCATATACATGGTTCTCTCCA
2801 GAGGTTTCATTACTGAACACTCGTCCGAGAATAACGAGTGGATCAGTCCTG

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105290-9002550

2851 GGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCCAATACTTTGGC  
2901 CACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTGATACTGGGAAA  
2951 GATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAAGAGTTGGATGG  
3001 AATACCAACTCGATGGACATGAGTTTGGACAGCTTCCAGGAGTTGGTA  
3051 ATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGTTGCAAAGAGTTG  
3101 GACACTACTGAGTGACTGAAGTGAAGTATAGTGTATCCATGGTACAGA  
3151 ATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTGAAGAGTTGTAG  
3201 GATATAAAAGTTTAGAATACCTTTAGTTTGAAGTCTTAAATTATTTACT  
3251 TAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTTAGAGACTGATG  
3301 TAGAGAGAATGAGCCCTGGCATAACCAGAAGCTAACAGCTATTGGTTATAG  
3351 CTGTTATAACCAATATAAGCAATATATGGTTATATAGCATGAAGCT  
3401 GATGCCAGCAATTTGAAGAACCAATTTAGAAGTATATCCTAAACTCTA  
3451 ATGTTCCAGGACACTGATCTTAAAGCTCAGGTTGAGAACTCTGTTTTATA  
3501 GGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCAGATGGTAAAGT  
3551 GTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGGCTTGGGAAGAT  
3601 CCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTTACCTGGAAAAT  
3651 TCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGGATGCAAAGAG  
3701 TTGAACACAACCTGAGCAACTAAGCACAGCACAGTACAGTATACACCTGTG  
3751 AGGTGAAGTGAAGTGAAGGTTCAATGCAGGCTCTCCTGCATTGCAGAAAG  
3801 ATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAACTACTGGAGTGGGT  
3851 AGCCTATTCTCTTCTCCAGGGGATCTTCCCATCCCAGGAATTTGAAGTGGAG  
3901 TCTCCTGCATTTAGGTGATTTCTTCCAGCTGAACCTACAGGTGGTAT  
3951 CTACTCCAATTATTAAGTGCTTAAAGTCCAGTTTCCCACCTTTCCCAA  
4001 AAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACTCTGAGGCTGTC  
4051 TACAAGCTTATATATTTATGAACACATTTATTGCAAGTTGTTAGTTTTAG  
4101 ATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTGGTTGGGGATGG  
4151 GGAGGCTGATAGCATCTCAGAGGGCAGCTAGACTGTGCATACACACTTT  
4201 TCAAGTCTCCATTTTGTGAAATGAAGAAGTCTCTGGATCTAAGTTATAT  
4251 GTGATTCTCAGTCTTGTGGTCATATTTCTATTCTACTCCTGACCACTCAA  
4301 CAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTCATGCCTGGGTTG  
4351 AGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGCTGGATTGGTTG  
4401 GACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGATGACATACACC  
4451 CCCCTTCCACATTTCTGCATGTCTTAGGGGGGAAGGGGAAGCTCGGTAT  
4501 AGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTATATTGCCCCAT  
4551 GCCCTTCTTTGTTTCTCAAGTAACCAGAGACAGTGCTTCCCAGAACCAAC  
4601 CCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAAGCAGGATCATG  
4651 GTTTGAACTCTTTCTGCCAGAGAACAAATACCTGCTATGGACTAGATACT  
4701 GGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGAAGCTGCCAGGC  
4751 TCAGCGTTTCTGTCTTGGCATGACCACTCTCTTCTATCTCTTCTCTAGA  
4801 TGTAGGGCTTGGTACCAGAGCCCTGAGGCTTCTGCATGAATATAAATA  
4851 TATGAACTGAGTGATGCTTCCATTTAGGTTCTTGGGGGCGCCGAATTC  
4901 GAGCTCGGTACCGGGGATCTCGACGGATCCGATTACTTACTGGCAGGTG  
4951 CTGGGGGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCT  
5001 CGACCAGGTTGAGATATCGGCGGGGACGCGCGGTGGTAATTACAAGG  
5051 AGATCCGATTACTTACTGCGAGGTGCTGGGGCTTCCGAGACAATCGCGA  
5101 ACATCTACACCACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGG  
5151 GACGCGGCGGTGGTAATTACAAGCGAGATCCCCGGGAATTGAGACCTCA  
5201 CCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGT  
5251 GTCCACTCCGAGGTCCAACCTGGTGGAGAGCGGTGGAGGTGTTGTGCAACC  
5301 TGGCCGGTCCCTCGCGCTGTCTGCTCCGCTGCTGGCTTCGATTCTACCA  
5351 CATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGTCTTGAGTGG  
5401 ATTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCT  
5451 AAAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCC  
5501 TGCAAATTGGACAGCTGAGACCCGAGAAGACACCGGGTCTATTTTTGTGCA  
5551 AGCCTTTACTTCGGCTTCCCCTGGTTGGCTTATGGGGCCAAGGGACCCC  
5601 GGTCAACGCTTCCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCTGG  
5651 CACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG  
5701 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAAGTACAGGCGC  
5751 CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTTACAGTCTCAGGAC  
5801 TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC  
5851 CAGACCTACATCTGCAACGTGAATCACAAGCCAGCAGCAACCAAGGTGGA  
5901 CAAGAGAGTTGAGCCCAAACTCTGTGACAAAACCTACACATGCCACCGC

Figure 10c

5951 GCCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCA  
6001 AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGT  
6051 GGTGGTGGACGTGAGCCAGAACCCCTGAGGTCAAGTTCAACTGGTACG  
6101 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAGCCGCGGGAGGACG  
6151 TACAACAGCAGCTACCGTGTGGTCAGCGTCTCACCCTCTGCACAGGA  
6201 CTGGCTGAATGGCAAGGATACAAAGTCAAGGTCCAACAAGCCCTCC  
6251 CAGCCCCCATCGAGAAAACCATCTCCAAGGCCAAGGGCAGCCCCGAGAA  
6301 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA  
6351 GGTGAGCCTGACCTGCTGGTCAAAGGCTTCTATCCACGCGACATCGCCG  
6401 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACACTACAAGACCACGCT  
6451 CCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTACCG  
6501 GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC  
6551 ACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCC  
6601 GGGAAATGAAAGCCGAATTGCCCCCTCTCCCTCCCCCCCCCTAACGTTA  
6651 CTGGCCGAAGCCGCTTGGGAATAAGGCCGGTGTGCGCTTTGTCTATATGTTA  
6701 TTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGCCCGGAAACCTGG  
6751 CCCTGTCTTCTTGACAGCATCTCTAGGGGTCTTCCCTCTCGCCAAAG  
6801 GAATGCAAGGTCTGTTGAATGTGCTGAAGGAAGCAGTTCTCTGGAAGCT  
6851 TCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCC  
6901 CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA  
6951 CACCTGCAAAGGGCCACAACCCCAAGTGCCACGTTGTGAGTTGGATAGTT  
7001 GTGGAAGAGTCAAATGGCTCTCTCAAGCGTATTCACAAGGGGCTGAA  
7051 GGATGCCCAAGAGTACCCCATGTATGGGATCTGATCTGGGGCTCGGT  
7101 GCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAACGCTCTAGGCCCC  
7151 CCGAACCACGGGGACGTGGTTTTCTTTGAAAAACACGATGATAATATGG  
7201 CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATCCATGCCACCCAG  
7251 GCCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGG  
7301 TGACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTG  
7351 TAGCCTGGTACCAGCAGGAAGCCAGGTAAGGCTCAAAGCTGCTGATCTAC  
7401 TGGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTACGCGGTAGCGG  
7451 TAGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACA  
7501 TCGCCCACTACTACTGCCAGCAATATAGCCTCTATCGGTGCTTCGGCCAA  
7551 GGGACCAAGGTGGAATCAAACGAAGTGTGGCTGCACCATCTGCTTTTCAT  
7601 CTTCCCGCATCTGATGAGCAGTTGAATCTGGAACTGCCCTCTGTTGTGT  
7651 GCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTG  
7701 GATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTACAGAGCAGGA  
7751 CAGCAAGGACAGCACTACAGCCTCAGCAGCACCTGACGCTGAGCAAAG  
7801 CAGACTACGAGAAACACAAAGTCTACGCTGCGGAAGTCACCCATCAGGGC  
7851 CTGAGCTCGCCGCTGACAAAGAGCTTCAACAGGGGAGAGTGTAGAGATC  
7901 CCCCCGGCTCGAGGAATTCGATATCAAGCTTATCGATAATCAACCTCTGG  
7951 ATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACATATGTTGCTCCT  
8001 TTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGC  
8051 TTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGT  
8101 CTCTTTTATGAGGATTGTGGCCCGCTTGTGAGGCAACGTGGCGGTGGTGTG  
8151 ACTGTTTGTGCTGAGTACCCCCCACTGGTTGGGGATTGCCACCACCTG  
8201 TCAGCTCCTTTCGGGCACTTTCGCTTTCCCCCTCCTATTGCCACGGCGG  
8251 AACTCATCGCCGCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTG  
8301 GGCATGACAATTCCTGGTGTGTGCGGGAAATCATCGTCTTTCTCTTG  
8351 GCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGAGCTCCTTCTGCT  
8401 ACGTCCCTTCGGCCCTCAATCCAGCGGACTCTCCTCCCGCGGCTCTGCT  
8451 CCGGCTCTGCGGCCTTCTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCG  
8501 GATCTCCCTTTGGGCCGCTCCCCGCTGATCGATACCGTCAACATCGAT  
8551 AAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGAATGAAAGACC  
8601 CCACCTGTAGGTTTGCAAGCTAGCTTAAGTAACGCCATTTGCAAGGCA  
8651 TGGAAAAACATAAATGAGAATAGAGAGTTTCAAGTCAAGGTCAGGAAT  
8701 AGATGGAACATGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCACT  
8751 CCTGCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCA  
8801 AACAGGATATCTGTGGTAAGCAGTTCTGCCCCGGCTCAGGGCCAAGAAC  
8851 AGATGGTCCCCAGATCGGCTCCAGCCCTCAGCAGTTCTAGAGAACCATC  
8901 AGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTT  
8951 GAACTAACCAATCAGTTGCTTCTGCTTCTGTCGCGGCTCTGCTCTC  
9001 CCGAGCTCAATAAAAGAGCGCCACAACCCCTCACTCGGGGCGCCAGTCTCT

9051 CGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCCTCTTGCA  
9101 GTTGCATCCGACTTGTGGTCTCGCTGTTCTTGGGAGGGTCTCCTCTGAG  
9151 TGATTGACTACCCGTACGCGGGGGTCTTTTCAAT

Variable	Mean	SD	Min	Max
Age	38.5	12.5	25	65
Gender	0.5	0.5	0	1
Marital status	0.7	0.5	0	1
Education	12.5	2.5	9	16
Income	3500	1500	1000	8000
Health status	0.8	0.4	0	1
Exercise frequency	2.5	1.5	0	5
Stress level	4.5	1.5	1	7
Sleep quality	3.5	1.5	1	6
Diet quality	4.0	1.5	1	6
Work-life balance	3.0	1.5	1	5
Family support	4.5	1.5	1	6
Community involvement	2.0	1.5	0	4
Life satisfaction	5.5	1.5	1	7
Overall well-being	4.0	1.5	1	6

**Figure 11a**  
**SEQ ID NO:8**  
**Alpha-Lactalbumin Bot Vector**

1 GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC  
51 AATACTTTGGCCACCTGATGCGAAGAAGTCACTCATGTGATAAGACCCTG  
101 ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA  
151 GAGTTGGATGGAATCACCACCTCGATGGACATGAGTTTGAGCAAGCTTCC  
201 AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT  
251 GCAAAGAGTTGGACACTACTGAGTGAAGTGAAGTGAAGTGAAGTGAAGT  
301 CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGGCCTGATTCTG  
351 AAGAGTTGTAGGATATAAAGTTTGAATACCTTTAGTTTGGAAAGTCTTA  
401 AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT  
451 AGAGACTGATGTAGAGAGAATGAGCCCTGGCATAACCAGAAGCTAACAGCT  
501 ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA  
551 GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAAGTATATC  
601 CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTTCAAGT  
651 CTTGTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA  
701 GATGGTAAAGTGCTGCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG  
751 CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT  
801 ACCTGGAATAATCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG  
851 ATTGCAAAGAGTTGAACACAAGTGAAGTGAAGGTTCAATGCAGGCTCCTGC  
901 ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGCTCCTGC  
951 ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA  
1001 CTGGAGTGGGTAGCCTATTCTTCTCCAGGGATCTTCCATCCCAGGAA  
1051 TTGAAGTGGAGTCTCCTGCATTTTCAAGTGGATTCTTCAACAGCTGAAGT  
1101 CCAGGTGGATACTACTCAATATTAAGTGCTTAAAGTCCAGTTTCCCA  
1151 CCTTCCCAAAAGGTTGGGTCACTCTTTTTTAACTTCTGTGGCCTACT  
1201 CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGT  
1251 GTTAGTTTTAGATTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG  
1301 GTTGGGGATGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC  
1351 ATACACACTTTTCAAGTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT  
1401 CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC  
1451 TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTC  
1501 TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTACATGGC  
1551 TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA  
1601 TGACATACACCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGG  
1651 AAGCTCGGTATAGAACCCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT  
1701 ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC  
1751 CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA  
1801 GCAGGATCATGGTTTGAAGTCTTCTGGCCAGAGAACAATACCTGCTATG  
1851 GACTAGATACTGGGAGAGGAAAGGAAAGTAGGGTGAATTATGGAAGGA  
1901 AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACAGTCTCTCTTCATT  
1951 CTCTTCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT  
2001 GAATATAAATATATGAACTGAGTGTGCTTCCATTTTCAAGTTCTTGGGG  
2051 GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGACGGATCCGATTACTT  
2101 ACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGGAACATCTACACCACA  
2151 CAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGACGCGCGGTGGT  
2201 AATTACAAGCGAGATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGA  
2251 GACAATCGCGAACATCTACACCACACAACACCGCCTCGACCAGGGTGAGA  
2301 TATCGGCCGGGACGCGCGGTGGTAATTACAAGCGAGATCTCGAGAAGC  
2351 TTGTTGGGAATTCAGGCCATCGATCCCGCCGCCACCATGGAATGGAGCTG  
2401 GGTCTTTCTCTTCTTCTGTGTAAGTACAGGTGTCCACTCCGACATCC  
2451 AGATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAACTGTC  
2501 ACTATCAGATGTGAGCAAGTGGGAATATTCACAATTATTTAGCATGGTA  
2551 TCAGCAGAAACAGGGAATCTCCTCAGCTCCTGGTCTATAATGCAAAAA  
2601 CCTTAGCAGATGGTGTGCCATCAAGTTTCAAGTGGCAGTGGATCAGGAACA  
2651 CAATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTA  
2701 TTAGTGTCAACATTTTGGAGTACTCCGTGGACGTTCCGTGGAGGCACCA  
2751 AGCTGGAAATCAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCA  
2801 CCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTT

T06290-0006860



Figure 11b

2851 GAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCA  
2901 GTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAA  
2951 GACAGCACCTACAGCATGAGCAGCACCCCTCACATTGACCAAGGACGAGTA  
3001 TGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT  
3051 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTGAAAGCATCGATTT  
3101 CCCCTGAATTGCCCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAA  
3151 GCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACC  
3201 ATATTGCCGTCTTTTGGCAATGTGAGGGCCCCGAAACCTGGCCCTGTCTT  
3251 CTTGACGAGCATTCCTAGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAG  
3301 GTCTGTTGAATGTGCTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGA  
3351 CAAACAACGCTCTGTAGCGACCCTTTCAGGGCAGCGGAACCCCCACCTGG  
3401 CGACAGGTGCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAA  
3451 AGGCGGCACAACCCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGA  
3501 GTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCCA  
3551 GAAGGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCT  
3601 TTACATGTGTTTAGTCGAGGTTAAAAAACGTTCTAGGCCCCCGAACCAC  
3651 GGGGACGTGGTTTTCTTTGAAAAACACGATGATAATATGGCCTCCTTTG  
3701 TCTCTGTGTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGAGGTT  
3751 CAGCTTCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTCAA  
3801 GTTGTCTGCACAGCTTCTGGCTTCAACATTAAAGACACCTTTATGCACT  
3851 GGGTGAAGCAGAGGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGAT  
3901 CCTGCGAATGGGAATACTGAATATGACCCGAAGTTCCAGGGCAAGGCCAC  
3951 TATAACAGCAGACACATCCTCCAACACAGTCAACCTGCAGCTCAGCAGCC  
4001 TGACATCTGAGGACACTGCCGTCTATTACTGTGCTAGTGGAGGGGAAGTG  
4051 GGGTTTCCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCAGCCAA  
4101 AACGACACCCCCATCTGTCTATCCACTGGCCCCTGGATCTGCTGCCCAA  
4151 CTAACCTCCATGGTGACCCTGGGATGCCTGGTCAAGGGCTATTTCCCTGAG  
4201 CCAGTGACAGTGACCTGGAAGTCTGGATCCCTGTCCAGCGGTGTGCACAC  
4251 CTTCCAGCTGTCTGTCAGTTTGACCTCTACACTCTGAGCAGCTCAGTGA  
4301 CTGTCCCTCCAGCACCTGGCCCAGCGAGACCGTCACTGCAACGTTGCC  
4351 CACCCGCCAGCAGCACCAAGGTGGACAAGAAAATTGTGCCAGGGATTG  
4401 TACTAGTGGAGGTGGAGGTAGCCACCATCACCATCACCATTAATCTAGAG  
4451 TTAAGCGGCCGTGAGATCTCGACATCGATAATCAACCTCTGGATTACAA  
4501 AATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGC  
4551 TATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGT  
4601 ATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTGTCTGTCTTTA  
4651 TGAGGAGTTGTGGCCCGTTGTGAGGCAACGTGGCGTGGTGTGCACTGTGT  
4701 TTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACTGTGAGCTC  
4751 CTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAAGTCA  
4801 CGCCGCTGCTTGGCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTG  
4851 ACAATTCCGTGGTGTGTGCGGGAAATCATCGTCTTTCTTGGCTGCTC  
4901 GCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCTTCTGCTACGTCCC  
4951 TTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCTGCTGCCGGCTC  
5001 TGCGGCTCTTCCGCGTCTTCCGCTTCCGCTCAGACGAGTCGGATCTCC  
5051 CTTTGGGCGCCTCCCCGCTGATCGATAAAATAAAAGATTTTATTTAGT  
5101 CTCCAGAAAAAGGGGGGAATGAAAGACCCACCTGTAGGTTTGGCAAGCT  
5151 AGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAA  
5201 TAGAGAAGTTCAGATCAAGGTGAGGAACAGATGGAACAGCTGAATATGGG  
5251 CCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGCTCAGGGCCAAG  
5301 AACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCA  
5351 GTTCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCC  
5401 AGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAA  
5451 GGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTT  
5501 CTCGCTTCTGTTGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCA  
5551 CAACCCCTCAGTCGGGGCGCCAGTCTCCGATTGACTGAGTCGCCCCGGGT  
5601 ACCCGGTATCCAATAAACCTCTTGCAGTTGCATCCGACTTGTGGTCTC

106290-90045860

**Figure 11c**

5651 GCTGTTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGG  
5701 GGTCTTTCATT

1 - 2053	Bovine/human alpha-lactalbumin 5' flanking region
2093 - 2336	Double mtated PPE sequence
2387 - 2443	cc49 signal peptide coding region
2444 - 3088	Bot antibody light chain Fab coding region
3112 - 3686	EMCV IRES
3687 - 3745	Bovine alpha-lactalbumin signal peptide coding region
3746 - 4443	Bot antibody heavy chain Fab coding region
4481 - 5072	WPRE sequence
5118 - 5711	Moloney murine leukemia virus 3' LTR

09697005-062901

**Figure 12a**  
**SEQ ID NO:9**  
**LSNRL Vector**

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1      TTTGAAAGACCCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTT
51     TGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAG
101    GTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGC
151    GGTTCTCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATG
201    GGCCAAACAGGATATCTGTGGTAAGCAGTTCTGCCCCGGCTCGGGGCCA
251    AGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA
301    TCATCAGATGTTTCCAGGTGCCCAAGGACCTGAAAATGACCCTGTACC
351    TTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTC
401    CGCTCTCCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGCGCGCCA
451    GTCTTCCGATAGACTGCGTCGCCCCGGGTACCCGTATTCCCAATAAAGCCT
501    CTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCTTGGGAGGGTCTC
551    CTCTGAGTGATTGACTACCCACGACGGGGTCTTTTCATTTGGGGGCTCGT
601    CCGGGATTTGGAGACCCCTGCCAGGGACCACCGACCCACCACCGGGAGG
651    TAAGCTGGCCAGCAACTTATCTGTCTGTCCGATTGTCTAGTGTCTATG
701    TTTGATGTTATCGCGCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTAT
751    CTGGCGGACCCGTGGTGGAAGTACGAGTTCTGAACACCCGGCCGCAACC
801    CTGGGAGACGTCCCAGGGACTTTGGGGGCCGTTTGTGGCCCGACCTGA
851    GGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGT
901    AGGAGACGAGAACCTAAAACAGTTCGCCCTCCGTCTGAATTTTGCCTTT
951    CGGTTTGAACCGAAGCCGCGCTCTTGTCTGCTGCAGCCAAGCTTGGGC
1001   TGCAGGTCGAGGACTGGGGACCCTGCACCGAATGAGAGAACACAACATC
1051   AGGATTCCTAGGACCCCTGCTCGTGTACAGGCGGGGTTTTCTTGTGTA
1101   CAAGAATCCTCACAATACCACAGAGTCTAGACTCGTGGTGGACTTCTCTC
1151   AATTTTCTAGGGGGAGCACCCACGTGTCTGGCCAAAATTTCGCAGTCCCC
1201   AACCTCCAATCACTCACCACCTCTTGTCTCCAATTTGTCTGGCTATC
1251   GCTGGATGTGTCTGCGGCGTTTTATCATATTCTCTTCATCCTGCTGCTA
1301   TGCCTCATCTTCTTGTGGTCTTCTGGACTACCAAGGTATGTTGCCCGT
1351   TTGTCCTCTACTTCCAGGAACATCAACTACCAGCACGGGACCATGCAAGA
1401   CCTGCACGATTCTGCTCAAGGAACCTCTATGTTTCCCTCTTGTGCTGT
1451   ACAAAACCTTCGGACGGAACCTGCACTTGTATTCCCATCCCATCATCCTG
1501   GGCTTTTCGAAGATTCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGC
1551   TCAGTTTACTAGTGCCATTGTTTCAGTGGTTCGTAGGGCTTTCCCCACT
1601   GTTTGGCTTTCAGTTATATGGATGATGTGGTATTGGGGCCAAGTCTGTA
1651   CAACATCTTGAGTCCCTTTTTACCTCTATTACCAATTTCTTTTGTCTTT
1701   GGGTATACATTTAAACCCTAATAAAACCAAACGTTGGGGCTACTCCCTTA
1751   ACTTCATGGGATATGTAATTGGATGTTGGGGTACTTTACCGCAAGAACAT
1801   ATTGTAATAAAATCAAGCAATGTTTTCGAAAAGTGCCTGTAAATAGACC
1851   TATTGATTGGAAGTATGTCAGAGACTTGTGGGTCTTTTGGGCTTTGCTG
1901   CCCCTTTTACACAATGTGGCTATCCTGCCTTAATGCCTTTATATGCATGT
1951   ATACAATCTAAGCAGGCTTTCACCTTCTCGCCAACTTACAAGGCCTTTCT
2001   GTGTAAACAATATCTGAACCTTTACCCCGTTGCCCGGCAACGGTCAGGTC
2051   TCTGCCAAGTGTGCTGACGCAACCCCACTGGATGGGGCTTGGCTATC
2101   GGCCATAGCCGCATGCGCGGACCTTTGTGGCTCCTCTGCCGATCCATACT
2151   GCGGAACCTCCTAGCAGCTTGTGTTGCTCGCAGGCGGTCTGGAGCGAACT
2201   TATCGGCACCGACAACCTCTGTTGTCTCTCTCGGAAATACACCTCCTTTC
2251   CATGGCTGCTAGGGTGTGCTGCCAACTGGATCCCCTCAGGATATAGTAGT
2301   TTCGCTTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACACTTGT
2351   AGTCTTGCAACATGGTAACGATGAGTTAGCAACATGCCTTACAAGGAGAG
2401   AAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTACGATCGTGC
2451   CTTATTAGGAAGGCAACAGACAGGTCTGACATGGATTGGACGAACCACTG
2501   AATTCCGCATTGTCAGAGATAATTGTATTTAAGTGCCTAGCTCGATACAGC
2551   AAACGCCATTTTTGACCATTACCCACATGGTGTGCACCTTCCAAAGCTT
2601   CACGCTGCCGCAAGCACTCAGGGCGCAAGGGCTGCTAAAGGAAGCGGAAC
2651   ACGTAGAAAGCCAGTCCGCAGAAACGGTGTGACCCCGGATGAATGTCAG
2701   CTACTGGGCTATCTGGACAAGGGAACGCAAGCGCAAGAGAGAAGCAGG
2751   TAGCTTGCAGTGGGCTTACATGGCGATAGCTAGACTGGGCGGTTTTATGG
2801   ACAGCAAGCGAACCAGGAATTGCCAGCTGGGGCGCCCTCTGGTAAGGTTGG

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TC250-9002550

Figure 12b

2851 GAAGCCCTGCAAAGTAAACTGGATGGCTTTCTTGCCGCCAAGGATCTGAT  
 2901 GGCGCAGGGGATCAAGATCTGATCAAGAGACAGGATGAGGATCGTTTCGC  
 2951 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGA  
 3001 GAGGCTATTCCGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATG  
 3051 CCGCCGTGTTCCGGCTGTCAGCGCAGGGCGCCCGGTTCTTTTTGTCAAG  
 3101 ACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCT  
 3151 ATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTG  
 3201 TCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  
 3251 GATCTCCTGTCTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGC  
 3301 TGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCG  
 3351 ACCACCAAGCGAAACATCGCATCGAGCGAGCACGTA CT CGGATGGAAGCC  
 3401 GGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCC  
 3451 AGCCGAACCTGTTCCGCCAGGCTCAAGCGCGCATGCCCGACGGCGAGGATC  
 3501 TCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAAT  
 3551 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCG  
 3601 CTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCG  
 3651 GCGAATGGGCTGACCGCTTCTCTCGTGCTTTACGGTATCGCCGCTCCCGAT  
 3701 TCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGG  
 3751 ACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACG  
 3801 AGATTTTCGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCG  
 3851 TTTTCCGGGACGCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTG  
 3901 GAGTTCCTTCGCCCACCCCAACCCTGGCCCTATTATTGGGTGGACTAACCA  
 3951 TGGGGGGAATTGCCGCTGGAATAGGAACAGGGACTACTGCTCTAATGGCC  
 4001 ACTCAGCAATTCCAGCAGCTCCAAGCCGAGTACAGGATGATCTCAGGGA  
 4051 GGTGAAAAATCAATCTCTAACCTAGAAAAGTCTCTCACTTCCCTGTCTG  
 4101 AAGTTGTCTACAGAATCGAAGGGGCTAGACTTGTTATTTCTAAAAGAA  
 4151 GGAGGGCTGTGTGCTGCTCTAAAAGAAGAATGTTGCTTCTATGCGGACCA  
 4201 CACAGGACTAGTGAGAGACAGCATGGCCAAATTGAGAGAGAGGCTTAATC  
 4251 AGAGACAGAAACTGTTTGAGTCAACTCAAGGATGGTTTGAGGGACTGTTT  
 4301 AACAGATCCCCTTGTTTACCACCTTGATATCTACCATTATGGGACCCCT  
 4351 CATTGTACTCCTAATGATTTTGCTCTTCGGACCCTGCATTCTTAATCGAT  
 4401 TAGTCCAATTTGTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTGTG  
 4451 ACTCAACAATATCACCAGCTGAAGCCTATAGAGTACGAGCCATAGATAAA  
 4501 ATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCA  
 4551 CCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGG  
 4601 AAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTGAGGAACAGA  
 4651 TGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCT  
 4701 GCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAAC  
 4751 AGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGA  
 4801 TGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGA  
 4851 TGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAA  
 4901 CTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCTGCTCCCCG  
 4951 AGCTCAATAAAAGAGCCCAACAACCCCTCACTCGGGGCGCCAGTCTCCGA  
 5001 TTGACTGAGTCGCGCGGTTACCCGTGATCCAATAAACCCCTCTTGCAAGTT  
 5051 GCATCCGACTTGTGGTCTCGCTGTTTCCTTGGGAGGGTCTCCTCTGAGTGA  
 5101 TTGACTACCCGTGACGCGGGGTCTTTCATT

1 - 589 MoMuSV 5' LTR  
 659 - 897 Retroviral packaging region  
 1034 - 1714 Hepatitis B surface antigen  
 2279 - 2595 RSV promoter  
 2951 - 3745 Neomycin phosphotransferase gene  
 4537 - 5130 MoMuLV 3' LTR

**Figure 13a**  
**SEQ ID NO:10**  
**Alpha-Lactalbumin cc49IL2 Vector**

1 GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC  
51 AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG  
101 ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA  
151 GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAAGCAAGCTTCC  
201 AGGAGTTGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT  
251 GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC  
301 CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG  
351 AAGAGTTGTAGGATATAAAAGTTTGAATAACCTTTAGTTTGAAGTCTTA  
401 AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT  
451 AGAGACTGATGTAGAGAGAATGAGCCCTGGCATAACCAGAAGCTAACAGCT  
501 ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA  
551 GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAAGTATATC  
601 CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTTCAAGT  
651 CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA  
701 GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG  
751 CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT  
801 ACCTGGAAAATTCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG  
851 ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT  
901 ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCATGCAGGGTCTCCTGC  
951 ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA  
1001 CTGGAGTGGGTAGCCTATTCCCTTCTCCAGGGGATCTTCCCATCCCAGGAA  
1051 TTGAAGTGGAGTCTCCTGCATTTCCAGGTGGATTCTTACCAGCTGAACCTA  
1101 CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA  
1151 CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT  
1201 CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT  
1251 GTTAGTTTTAGATTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG  
1301 GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC  
1351 ATACACACTTTTCAAGTTCTCCATTTTGTGAAATAGAAAGTCTCTGGAT  
1401 CTAAGTTATATGTGATTCTCAGTCTCTGTGCTCATATTCTATTCTACTCC  
1451 TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA  
1501 TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC  
1551 TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA  
1601 TGACATACACCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG  
1651 AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT  
1701 ATTGCCCCCATGCCCTTCTTTGTCTCAAGTAACCAGAGACAGTGCTTC  
1751 CCAGAACCAACCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA  
1801 GCAGGATCATGTTTTGAAGTCTTTCTGGCCAGAGAACAATACCTGCTATG  
1851 GACTAGATACTGGGAGAGGGAAGGAAAAGTAGGGTGAATTATGGAAGGA  
1901 AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT  
1951 CTCTTCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTCTGCAT  
2001 GAATATAAATATATGAACTGAGTGATGCTTCCATTTCAAGTTCTTGGGG  
2051 GCGCCGAATTTCGAGCTCGGTACCCGGGGATCTCGAGAAGCTTTAACCATG  
2101 GAATGGAGCTGGGTCTTCTCTTCTTCTGTCTCAGTAACTACAGGTGTCCA  
2151 CTCCCAGGTTCAAGTTGCAGCAGTCTGACGCTGAGTTGGTGAAACCTGGGG  
2201 CTTCAAGTGAAGATTTCTGCAAGGCTTCTGGCTACACCTTCACTGACCAT  
2251 GCAATTCACTGGGTGAAACAGAACCCTGAACAGGGCCTGGAATGGATTGG  
2301 ATATTTTTCTCCCGGAAATGATGATTTTAAATACAATGAGAGGTTCAAGG  
2351 GCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACTGCCTACGTGCAG  
2401 CTCAACAGCCTGACATCTGAGGATTCTGCAGTGTATTTCTGTACAAGATC  
2451 CCTGAATATGGCCTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAG  
2501 GAGGCGGAGGCGGAGGCGGTGGCTCGGGAGGCGGAGGCTCGGACATT  
2551 GTGATGTCACAGTCTCCATCCTCCCTACCTGTGTGAGTTGGCGAGAAGGT  
2601 TACTTTGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTGGTAATCAAA  
2651 AGAACTACTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTG  
2701 CTGATTTACTGGGCATCCGCTAGGGAATCTGGGGTCCCTGATCGCTTAC  
2751 AGGCAGTGGATCTGGGACAGATTTCACTCTCTCCATCAGCAGTGTGAAGA  
2801 CTGAAGACCTGGCAGTTTATTACTGTGAGCAGTATTATAGCTATCCCCTC

T05290-9004550

[illegible]

1 - 2055	Bovine/human alpha-lactalbumin 5' flanking region
2098 - 4011	cc49-IL2 coding region
4068 - 4661	MoMuLV 3' LTR

**Figure 14a**  
**SEQ ID NO:11**  
**Alpha-Lactalbumin YP Vector**

```

1   GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51  AATACTTTGGCCACCTGATGCCAAGAACTGACTCATGTGATAAGACCCTG
101 ATACTGGGAAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151 GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
201 AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251 GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301 CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351 AAGAGTTGTAGGATATAAAAGTTTGAATAACCTTTAGTTTGGAAGTCTTA
401 AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451 AGAGACTGATGTAGAGAGAATGAGCCCTGGCATAACCAGAAGCTAACAGCT
501 ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
551 GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAAGTACTATC
601 CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
651 CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701 GATGGTAAAGTGCTGCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
751 CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801 ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851 ATTGCAAAGAGTTGAACACAACCTGAGCAACTAAGCACAGCACAGTACAGT
901 ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
951 ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001 CTGGAGTGGGTAGCCTATTCTCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051 TTGAACTGGAGTCTCCTGCATTTTCAGGTGGATTCTTCACCAGCTGAACTA
1101 CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151 CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201 CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251 GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301 GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351 ATACACACTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401 CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451 TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501 TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551 TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601 TGACATACACCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651 AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701 ATTGCCCCCATGCCCTTCTTTGTTCTCAAGTAACCAGAGACAGTGCTTC
1751 CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801 GCAGGATCATGGTTTGAAGTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851 GACTAGATACTGGGAGAGGGAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901 AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951 CTCTTCTAGATGTAGGGCTTGGTACCAGAGCCCTGAGGCTTTCTGCAT
2001 GAATATAAATATATGAACTGAGTGATGCTTCCATTTAGGTTCTTGGGG
2051 GCGCCGAATTTCGAGCTCGGTACCCGGGGATCTCGACGGATCCGATTACTT
2101 ACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAACATCTACACCACA
2151 CAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGT
2201 AATTACAAGCGAGATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGA
2251 GACAATCGCGAACATCTACACCACACAACACCGCCTCGACCAGGGTGAGA
2301 TATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCGAGATCTCGAGTTAA
2351 CAGATCTAGGCCTCTAGGTGACGGATCCCCGGGAATTCGGCGCCGCCA
2401 CCATGATGTCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCC
2451 ACCCAGGCCCCAGGTTCAACTGCAGCAGTCTGGGCCTGAGCTGGTGAAGCC
2501 TGGGACTTCAGTGAGGATATCTTGCAAGGCTTCTGGCTACACCTTCACAA
2551 GCTACTATTTTACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGG
2601 ATTGCATGGATTTATCCTGGAAATGTTATTACTACGTACAATGAGAAGTT
2651 CAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACA
2701 TGCACCTCAACAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCA
2751 AGGGGTGACCATGATCTTGACTACTGGGGCCAAGGCACCACTCTCACAGT
2801 CTCCTCAGCCAAAACGACACCCCCATCTGTCTATCCACTGGCCCCCTGGAT

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F06290-90026860

Figure 14b

2851 CTGCTGCCCCAACTAACTCCATGGTGACCCTGGGATGCCTGGTCAAGGGC  
2901 TATTTCCCTGAGCCAGTGACAGTGACCTGGAACCTCTGGATCCCTGTCCAG  
2951 CGGTGTGCACACCTTCCCAGCTGTCTGCAGTCTGACCTCTACACTCTGA  
3001 GCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCCAGCGAGACCGTCACC  
3051 TGCAACGTTGCCACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGT  
3101 GCCCAGGGATTGTACTAGTGGAGGTGGAGGTAGCTAAGGGAGATCTCGAC  
3151 GGATCCCCGGGAATTGCCCCCTCTCCCTCCCCCCCCCTAACGTTACTGG  
3201 CCGAAGCCGCTTGGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTT  
3251 CCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCCGGAACCTGGCCCT  
3301 GTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCTCTCGCCAAAGGAAT  
3351 GCAAGGTCTGTTGAATGTGCTGAAGGAAGCAGTTCCTCTGGAAGCTTCTT  
3401 GAAGACAAAACAGTCTGTAGCGACCCTTGCAGGCAGCGGAACCCCCCA  
3451 CCTGGCGACAGGTGCCTCTGCGGCCAAAGCCACGTGTATAAGATACACC  
3501 TGCAAAGGCGGCACAACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGG  
3551 AAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGAT  
3601 GCCCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGCAC  
3651 ATGCTTTACATGTGTTTAGTTCGAGGTTAAAAAACGTTAGGCCCCCCGA  
3701 ACCACGGGGACGTGGTTTTCTTTGAAAAACAGATGATAATATGGCCTC  
3751 CTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCG  
3801 ACATTGTGCTGACACAATCTCCAGCAATCATGTCTGCATCTCCAGGGGAG  
3851 AAGGTACCCATGACCTGCAGTGCCACCTCAAGTGTAAGTTACATACACTG  
3901 GTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACAT  
3951 CCAAACCTGGCTTCTGGAGTCCCTGCTCGCTCAGTGGCAGTGGGTCTGGG  
4001 ACCTCTCACTCTCTCACTCAGCAGCATGGAGGCTGAAGATGCTGCCAC  
4051 TTATTACTGCCAGCAGTGGGGTAGTTACCTCACGTTCCGGTGGGGGACCA  
4101 AGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCA  
4151 CCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTT  
4201 GAACAACCTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCA  
4251 GTGAACGACAAAATGGCGTCTGAACAGTTGGACTGATCAGGACAGCAAA  
4301 GACAGCACCTACAGCATGAGCAGCACCTCACGTTGACCAAGGACGAGTA  
4351 TGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT  
4401 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAATAGGGGAGATCT  
4451 CGACATCGATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTG  
4501 GTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTA  
4551 ATGCCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTTCAATTTCTCCTC  
4601 CTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTG  
4651 TCAGGCAACGTGGCGTGGTGTGCACTGTGTTTGTGACGCAACCCCCACT  
4701 GGTGGGGCATTGCCACCACCTGTGAGCTCCTTTCCGGGACTTTGCTTTT  
4751 CCCCCCTCCTATTGCCACGGCGGAACATCATCGCCGCTGCCTTGCCCGCT  
4801 GCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCGGTGGTGTGTCG  
4851 GGGAAATCATCGTCCTTTTCTTGGCTGCTCGCCTGTGTTGCCACCTGGAT  
4901 TCTGCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCAGCGG  
4951 ACCTTCTTCCCCGCGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTT  
5001 CGCCTTCGCCCTCAGACGAGTCGGATCTCCCTTTGGGCGCCTCCCCGCC  
5051 TGATCGATAAAAATAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGAAT  
5101 GAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTT  
5151 GCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTAGATCAAGG  
5201 TCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGT  
5251 AAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAAT  
5301 ATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGG  
5351 CCAAGAACAGATGGTCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGA  
5401 GAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTG  
5451 CCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTGCGCGCT  
5501 TCTGCTCCCCGAGCTCAATAAAAGAGCCACAACCCCTCACTCGGGGCGC  
5551 CAGTCCTCCGATTGACTGAGTCGCCCCGGGTACCCGTGTATCCAATAAAC  
5601 CTCTTGACAGTTGCATCCGACTTGTGGTCTCGCTGTTCTTGGGAGGGTCT



**Figure 14c**

5651 CCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATT

1 - 2053	Bovine/Human Alpha-lactalbumin 5' flanking region
2093 - 2336	Double mutated PPE sequence
2403 - 2459	Bovine alpha-lactalbumin signal peptide coding region
2460 - 3137	Yersenia pestis heavy chain Fab gene coding region
3167 - 3742	EMCV IRES
3743 - 3799	Bovine alpha-lactalbumin signal peptide coding region
3800 - 4441	Yersenia pestis light chain Fab gene coding region
4461 - 5052	WPRE sequence
5098 - 5691	Moloney murine leukemia virus 3' LTR

T05290" 90046860

**Figure 15**  
**SEQ ID NO:12**  
**IRES-Casein Signal Peptide Sequence**

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1      GGAATTGCCCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCG
51     CTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATAT
101    TGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTG
151    ACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT
201    GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAA
251    CAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGAC
301    AGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGC
351    GGCACAACCCCAAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCA
401    AATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAG
451    GTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC
501    ATGTGTTTtagTCGAGGTTAAAAAACGTCTAGGCCCCCGAACCACGGGG
551    ACGTGGTTTTCTTTGAAAAACACGATGATAATATGGCCTTGCTCATCCT
601    TACCTGTCTTGTGGCTGTTGCTCTTGCCGGCGCCATGGGATATCTAGATC
651    TCGAGCTCGCGAAAGCTT

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1 - 583	IRES
584 - 628	Modified bovine alpha-S1 casein signal peptide coding region
629 - 668	Multiple cloning site

T:06290" 90026860

Figure 16a

SEQ ID NO: 13

LNBOEDC Vector

1 TTTGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTT  
51 TGCAAGGCATGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAG  
101 GTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGC  
151 GGTTCCCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATG  
201 GGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCA  
251 AGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA  
301 TCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCTGTACC  
351 TTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTC  
401 CGCTCTCCGAGCTCAATAAAAGAGCCCCACAACCCCTCACTCGGCGCGCCA  
451 GTCTTCCGATAGACTGCGTCGCCCCGGGTACCCGTATTCCCAATAAAGCCT  
501 CTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCTTGGGAGGGTCTC  
551 CTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGT  
601 CCGGAGATTGGAGACCCCTGCCAGGGACCACCGACCCACCACCGGGAGG  
651 TAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATG  
701 TTTGATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTAT  
751 CTGGCGGACCCGTGGTGGAACTGACGAGTCTGAACACCCGGCCGCAACC  
801 CTGGGAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGA  
851 GGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTCTGGT  
901 AGGAGACGAGAACCTAAACAGTTCCTGCTCCGTCTGAATTTTGTCTTT  
951 CGGTTTTGGAACCGAAGCCGCGCTCTGTCTGCTGCAGCGCTGCAGCATC  
1001 GTTCTGTGTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTA  
1051 GGGCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAG  
1101 ATGTCGAGCGGATCGCTCACAACCAAGTCGGTAGATGTCAAGAAGAGACGT  
1151 TGGGTTACCTTCTGCTCTGCAGAAATGGCCAACCTTTAACGTCGGATGGCC  
1201 GCGAGACGGCACCTTTAACCGAGACCTCATCAACAGGTTAAGATCAAGG  
1251 TCTTTTACCTTGCCCGCATGGACACCCAGACCAAGGTCCCTACATCGTG  
1301 ACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGT  
1351 ACACCCTAAGCCTCCGCCTCCTCTTCTCCATCCGCCCCGTCTCTCCCCC  
1401 TTGAACCTCCTCGTTCGACCCCGCTCGATCCTCCCTTTATCCAGCCCTC  
1451 ACTCCTTCTCTAGGCGCCGGAATFCCGATCTGATCAAGAGACAGGATGAG  
1501 GATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCC  
1551 GCTTGGGTGGAGAGGCTATTCCGGCTATGACTGGGCACAACAGACAATCGG  
1601 CTGCTCTGATGCCGCCGTGTTCCGGCTGTGACGCGAGGGGCGCCCGGTTT  
1651 TTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGTGCAGGACGAG  
1701 GCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCAGAGCTGT  
1751 GCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAG  
1801 TGCCGGGGCAGGATCTCCTGTCTCATCTCACCTTGCTCCTGCCGAGAAAGTA  
1851 TCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTAC  
1901 CTGCCCATTTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTAATC  
1951 GGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAG  
2001 GGGCTCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCGCGCATGCCCGA  
2051 CGGCGAGGATCTCGTCTGACCCATGGCGATGCCTGCTTGCCGAATATCA  
2101 TGGTGGAAAATGGCCGCTTTTCTGGATTGATCGACTGTGGCCGGCTGGGT  
2151 GTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGA  
2201 AGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCGTGCTTTACGGTATCG  
2251 CCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTC  
2301 TTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCAAC  
2351 CTGCCATCACGAGATTTTCGATTCCACCGCCGCTTCTATGAAAGGTTGGG  
2401 CTTCCGAATCGTTTTCCGGGACGCGGCTGGATGATCCTCCAGCGCGGGG  
2451 ATCTCATGTGAGTTCCTTCGCCCCACCCGGGCTCGATCCCTCGCGAGT  
2501 TGGTTCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCA  
2551 GTGCAAATCCGTGCGCATCCAGGAAACAGCAGCGGCTATCCGCGCATCC  
2601 ATGCCCCCGAACTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAG  
2651 GCGGATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCA  
2701 ATATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTAC  
2751 ATTTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATT

09897006-062901

Figure 16b

2801 GACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCAT  
2851 ATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGA  
2901 CCGCCCAACGACCCCCGCCCATTTGACGTCAATAATGACGTATGTTCCCAT  
2951 AGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTAC  
3001 GGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACG  
3051 CCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCA  
3101 GTACATGACCTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAG  
3151 TCATCGCTATTACCATGGTGATGCGGTTTGGCAGTACATCAATGGGCGT  
3201 GGATAGCGGTTTGA CTACG GGGGATTTC CAAGTCTCCACCCCATTGACGT  
3251 CAATGGGAGTTTGT TTTTGGCACC AAAATCAACGGGACTTTCCAAAATGTC  
3301 GTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGG  
3351 GAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAG  
3401 ACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCA  
3451 GCCTCCGCGGCCCAAGCTTCTCGACGGATCCCGGGAAATTCAGGCCATC  
3501 GATCCCGCGGCCACCATGGAATGGAGCTGGGTCTTTCTCTTCTTCTGTC  
3551 AGTAACTACAGGTGTCCACTCCGACATCCAGATGACCCAGTCTCCAGCCT  
3601 CCCTATCTGCATCTGTGGGAGAACTGTCACTATCACATGTGCGAGCAAGT  
3651 GGGAATATTCACAATTATTTAGCATGGTATCAGCAGAAACAGGGAAAATC  
3701 TCCTCAGCTCCTGGTCTATAATGCAAAAACCTTAGCAGATGGTGTGCCAT  
3751 CAAGTTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAAC  
3801 AGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAG  
3851 TACTCCGTGGACGTTCCGGTGGAGGCACCAAGCTGGAAATCAAACGGGCTG  
3901 ATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACA  
3951 TCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACCTTACCCCAAAGA  
4001 CATCAATGTCAAGTGGAGATTGATGGCAGTGAACGACAAAATGGCGTCC  
4051 TGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGC  
4101 AGCACCTCACATTGACCAAGGACGAGTATGAACGACATAACAGCTATAC  
4151 CTGTGAGGCCACTCACAAGACATCAACTTACCCATTGTCAAGAGCTTCA  
4201 ACAGGAATGAGTGTGAAAGCATCGATTTCCTTGAATTGCCCCCTCTCC  
4251 CTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGAATAAGGCCGGT  
4301 GTGCGTTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAAT  
4351 GTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGG  
4401 TCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCTGTAAGG  
4451 AAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACC  
4501 CTTTGCAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTCTGCGGCCA  
4551 AAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAAGTCC  
4601 ACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGC  
4651 GTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCAATTGTATGGG  
4701 ATCTGATCTGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGT  
4751 TAAAAAACGCTCTAGGCCCCCGAACCACGGGGACGTGGTTTTCTTTTGA  
4801 AAAACACGATGATAATATGGCCTCCTTTGTCTCTCTGCTCCTGGTAGGCA  
4851 TCCTATTCCATGCCACCCAGGCCGAGGTTTCAAGCTTCAAGCAGTCTGGGGCA  
4901 GAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGTCTGACAGCTTCTGG  
4951 CTTCAACATTAAAGACACCTTATGCACTGGGTGAAGCAGAGGCCTGAAC  
5001 AGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGGAATACTGAA  
5051 TATGACCCGAAGTTCAGGGCAAGGCCACTATAACAGCAGACACATCCTC  
5101 CAACACAGTCAACCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCG  
5151 TCTATTACTGTGCTAGTGGAGGGGAACTGGGGTTTCTTACTGGGGCCAA  
5201 GGGACTCTGGTCACTGTCTCTGCAGCCAAAACGACACCCCATCTGTCTA  
5251 TCCACTGGCCCTGGATCTGCTGCCCAAATAACTCCATGGTGACCTGG  
5301 GATGCCCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAAC  
5351 TCTGGATCCCTGTCCAGCGGTGTGCACACCTTCCCAGCTGTCTGACGTC  
5401 TGACCTCTACACTCTGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGC  
5451 CCAGCGAGACCGTCACCTGCAACGTTGCCACCCGGCCAGCAGCACCAAG  
5501 GTGGACAAGAAAATTTGTCAGGGGATTGTACTAGTGGAGGTGGAGGTAG  
5551 CCACCATCACCATCACCATTAACTAGAGTTAAGCGGCCGTCGAGATCTA  
5601 GGCTCCTAGGTGACATCGATAAAATAAAAGATTTTATTTAGTCTCCAG  
5651 AAAAAGGGGGGAATGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTA  
5701 AGTAACGCCATTTTGAAGGCATGGAAAAATACATAACTGAGAATAGAGA  
5751 AGTTCAGATCAAGGTGAGGAACAGATGGAACAGCTGAATATGGGGCCAAAC  
5801 AGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGA  
5851 TGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCT

Figure 16c

5901 GCCCCGGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCT  
5951 CAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCT  
6001 GAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCT  
6051 TCTGTTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCC  
6101 CTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCCGGGTACCCGT  
6151 GTATCCAATAAACCCCTCTTGAGTTGCATCCGACTTGTGGTCTCGCTGTT  
6201 CCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTT  
TCATT

Moloney Murine Sarcoma Virus 5' LTR	1 - 589
Moloney Murine Leukemia Virus Extended Packaging Region	659 - 1468
Neomycin Resistance Gene	1512 - 2306
CMV Promoter	2656 - 3473
cc49 Signal Peptide Coding Region	3516 - 3572
Bot Fab 5 Light Chain	3573 - 4217
EMCV IRES (Clonotech)	4235 - 4816
Modified Bovine $\alpha$ -LA Signal Peptide Coding Region	4817 - 4873
Bot Fab 5 Heavy Chain	4874 - 5572
Moloney Murine Leukemia Virus 3' LTR	5662 - 6255

105290-9002550

Figure 17a  
SEQ ID NO: 34  
LNBOTDC Vector

1 GAATTAATTCATACCAGATCACCGAAAACGTCTCCAAATGTGTCCCCC  
51 TCACACTCCCAAATTCGCGGGCTTCTGCCTCTTAGACCACTCTACCCTAT  
101 TCCCCACACTCACCGGAGCCAAAGCCGCGGCCCTTCCGTTTCTTTGCTTT  
151 TGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTG  
201 CAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTTCAAGTCAAGGT  
251 CAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGG  
301 TTCTTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATGGG  
351 CCAAACAGGATATCTGTGGTAAGCAGTTCTTGCCCCGGCTCGGGGCCAAG  
401 AACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATC  
451 ATCAGATGTTTCCAGGTGCCCCAAGGACCTGAAAATGACCCTGTACCTT  
501 ATTTGAACTAACCAATCAGTTTCGCTTCTCGCTTCTGTTCGCGCGCTTCCG  
551 CTCTCCGAGCTCAATAAAAGAGCCACAACCCCTCACTCGGCGCGCCAGT  
601 CTTCCGATAGACTGCGTTCGCGGGTACCCGTATTCCCAATAAAGCCTCT  
651 TGCTGTTTGCATCCGAATCGTGCTCGCTGTTCTTGGGAGGGTCTCCT  
701 CTGAGTGATTGACTACCCACGACGGGGTCTTTTCAATTTGGGGGCTCGTCC  
751 GGGATTTGGAGACCCCTGCCAGGGACACCGACCCACCACCGGGAGGTA  
801 AGCTGGCCAGCAACTTATCTGTGCTGTGTCGATTGTCTAGTGTCTATGTT  
851 TGATGTTATGCGCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCT  
901 GCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGCGCAACCCCT  
951 GGGAGACGTCCAGGGACTTTGGGGGCGGTTTTTGTGGCCCGACCTGAGG  
1001 AAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGTAG  
1051 GAGACGAGAACCTAAACAGTTCCCGCCTCCGTCTGAATTTTGTCTTTCG  
1101 GTTTGGAACCGAAGCCGCGCGTCTGTGCTGCTGCAGCGCTGCAGCATCGT  
1151 TCTGTGTTGTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGG  
1201 GCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGTCTAGTGGAAAGAT  
1251 GTCGAGCGGATCGTCAACACAGTCGGTAGATGTCAAGAAGAGACGTTG  
1301 GGTACCTTCTGCTCTGCAGAAATGGCCAACCTTTAACGTCGGATGGCCGC  
1351 GAGACGGCACCTTTAACCGAGACCTCATCAACAGGTTAAGATCAAGGTC  
1401 TTTTACCTGGCCCGCATGGACACCCAGACAGGTCCCCTACATCGTGAC  
1451 CTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTAC  
1501 ACCCTAAGCCTCCGCTCCTCTTCTCCATCCGCCCCGTCTCTCCCCCTT  
1551 GAACCTCCTCGTTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCAC  
1601 TCCTTCTCTAGGCGCCGGAATTCGATCTGATCAAGAGACAGGATGAGGG  
1651 AGCTTGATATATCCATTTTCGGATCTGATCAGCACGTGTTGACAATTAATC  
1701 ATCGGCATAGTATATCGGCATAGTATAATACGACAAGGTGAGGAACTAAA  
1751 CCATGGCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTGAAAGAGCA  
1801 ACGGCTACAATCAACAGCATCCCCATCTCTGAAGACTACAGCGTCGCCAG  
1851 CGCAGCTCTCTCTAGCGACGGCCGATCTTCACTGGTGTCAATGTATATC  
1901 ATTTTACTGGGGGACCTTGTGCAGAACTCGTGGTGTGGGCACTGCTGCT  
1951 GCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCGATCGGAAATGAGAA  
2001 CAGGGGCATCTTGAGCCCTGCGGACGGTGTGACAGGTGCTTCTCGATC  
2051 TGCATCCTGGGATCAAAGCGATAGTGAAGGACAGTGATGGACAGCCGACG  
2101 GCAGTTGGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTA  
2151 AGCACTTCGTGGCCGAGGAGCAGGACTGACACGTGCTACGAGATTTTCGAT  
2201 TCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGA  
2251 CGCCGGCTGGATGATCCTCCAGCGCGGGATCTCATGCTGGAGTTCTTCG  
2301 CCCACCCCAACTTGTTTATGTCAGCTTATAATGGTTACAAATAAAGCAAT  
2351 AGCATCACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG  
2401 TGGTTTGTCCAACTCATCAATGTATCTTATCATGTCTGTACGAGTTGGT  
2451 TCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGC  
2501 AAATCCGTGCGCATCCAGGAAACCAGCAGCGGCTATCCGCGCATCCATGC  
2551 CCCCGAACCTGCAGGAGTGGGGAGGACGATGGCCGCTTTGGTTCGAGGCGG  
2601 ATCCGGCCATTAGCCATATTTATTCATTGGTTATATAGCATAAATCAATAT  
2651 TGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACATTT  
2701 ATATTGGCTATGTCACATTACCGCCATGTTGACATTGATTATTGACT  
2751 AGTTATTAATAGTAATCAATTACGGGGTCATTAGTTTCATAGCCCATATAT  
2801 GGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGC  
2851 CCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTA

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Figure 17b

2901 ACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTA  
 2951 AACTGCCCACCTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCC  
 3001 CTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCCAGTAC  
 3051 ATGACCTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAGTCAT  
 3101 CGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGAT  
 3151 AGCGGTTTGACTCACGGGGATTTCGAAGTCTCCACCCCAATTGACGTCAAT  
 3201 GGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTGCTAA  
 3251 CAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAGG  
 3301 TCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGACGC  
 3351 CATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCT  
 3401 CCGCGGCCCCCAAGCTTCTCGAGTTAACAGATCTAGGCTGGCAGACAGGT  
 3451 TTCCCGACTGGAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAG  
 3501 CTCACTCATTAGGCACCCAGGCTTTTACACTTTATGCTTCCGGCTCGTAT  
 3551 GTTGTGTGGAATTTGTGAGCGGATAACAATTTACACAGGAAACAGCTATG  
 3601 ACCATGATTACGCCAAGCTTGGCTGCAGGTCGACGGATCCACTAGTAACG  
 3651 GCGGCCAGTGTGCTGGAATTCACCATGGGGCAACCGGGAACGGCAGCGC  
 3701 CTTCTTGCTGGCACCCAATGGAAGCCATGCGCCGGACACGACGTCACGC  
 3751 AGCAAAGGGACGAGGTGTGGGTGGTGGGCATGGGCATCGTCATGTCTCTC  
 3801 ATCGTCTTGCCCATCGTGTTTGGCAATGTGCTGGTCATCACAGCCATTGC  
 3851 CAAGTTCGAGCGTCTGCAGACGGTCACCAACTACTTCATCACAGCTTGG  
 3901 CCTGTGCTGATCTGGTCATGGGGCTAGCAGTGGTGGCCTTTGGGGCCGCC  
 3951 CATATTCTCATGAAAATGTGGACTTTTGGCAACTTCTGGTGCGAGTTCTG  
 4001 GACTTCCATTGATGTGCTGTGCGTCACGGCATCGATTGAGACCCTGTGCG  
 4051 TGATCGCAGTCGACCGCTACTTTGCCATTACTAGTCCTTTCAAGTACCAG  
 4101 AGCCTGCTGACCAAGAATAAGGCCCGGGTGATCATTCTGATGGTGTGGAT  
 4151 TGTGTCAGGCCCTTACCTCCTTCTTGCCCATTCAGATGCACTGGTACAGGG  
 4201 CCACCCACCAGGAAGCCATCAACTGCTATGCCAATGAGACCTGCTGTGAC  
 4251 TTCTTCACGAACCAAGCCTATGCCATTGCCTCTTCCATCGTGTCTTCTA  
 4301 CGTTCCCCCTGGTGATCATGGTCTTCGTCTACTCCAGGGTCTTTCAGGAGG  
 4351 CCAAAAGGCAGCTCCAGAAGATTGACAAAATCTGAGGGCCGCTTCCATGTC  
 4401 CAGAACCTTAGCCAGGTGGAGCAGGATGGGCGGACGGGGCATGGACTCCG  
 4451 CAGATCTTCCAAGTTCTGCTTGAAGGAGCACAAAGCCCTCAAGACGTTAG  
 4501 GCATCATCATGGGCACCTTTCACCCCTCTGCTGGCTGCCCTTCTTCATCGTT  
 4551 AACATTGTGCATGTGATCCAGGATAACCTCATCCGTAAGGAAGTTTACAT  
 4601 CCTCCTAAATTGGATAGGCTATGTCAATTCTGGTTTCAATCCCTTATCT  
 4651 ACTGCCGGAGCCCAGATTTCAGGATTGCCTTCCAGGAGCTTCTGTGCCTG  
 4701 CGCAGGTCTTCTTTGAAGGCCTATGGCAATGGCTACTCCAGCAACGGCAA  
 4751 CACAGGGGAGCAGAGTGGATATCACGTGGAACAGGAGAAAGAAATAAAC  
 4801 TGCTGTGTGAAGACCTCCAGGCACGGAAGACTTTGTGGGCCATCAAGGT  
 4851 ACTGTGCCTAGCGATAACATTGATTACAAAGGGAGGAATTGTAGTACAAA  
 4901 TGACTCACTGCTCTCGAGAAATCGAGGGGCGGCACCACCATCATCACCACG  
 4951 TCGACCCCGGGGACTACAAGGATGACGATGACAAGTAAGCTTTATCCATC  
 5001 AACTTGGCGGCCGCTCGAGCATGCATCTAGCGGCCGCTCGAGGCCGGCAA  
 5051 GGCCGGATCCCCGGGAATTGCCCCCTCTCCCTCCCCCCCCCTAACGTTA  
 5101 CTGGCCGAAGCCGCTTGAATAAGGCCGGTGTGCGTTTGTCTATATGTTA  
 5151 TTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGG  
 5201 CCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCTCTCTGCCAAAG  
 5251 GAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCTCTGGAAGCT  
 5301 TCTTGAAGACAAACAACGTCTGTAGCGACCCCTTTGCAGGCAGCGGAACCC  
 5351 CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA  
 5401 CACCTGCAAAGGCGGCACAACCCCAAGTGCCACGTTGTGAGTTGGATAGTT  
 5451 GTGGAAAGAGTCAAATGGCTCTCTCAAGCGTATTCAACAAGGGGCTGAA  
 5501 GGATGCCCAGAAGGTACCCCATTTGATGGGATCTGATCTGGGGCCTCGGT  
 5551 GCACATGCTTTACATGTGTTAGTCGAGGTTAAAAAACGTTAGGCCCCC  
 5601 CCGAACCACGGGGACGTGGTTTTCTTTGAAAAACACGATGATAATATGG  
 5651 CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTTCCATGCCACCCAG  
 5701 GCGGAGCTCACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAG  
 5751 GGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTGTACAGCTCCAACA  
 5801 ATAAGAACTATTTAGCTTGGTATCAGCAGAAACCAGGACAGCCTCCTAAG  
 5851 CTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT  
 5901 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGC  
 5951 AGGCTGAAGATGTGGCAGTTTATTACTGTGAGCAATATTATAGTACTCAG

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Figure 17c

6001 ACGTTTCGGCCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACC  
6051 ATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGT  
6101 CCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGGCCAAAGTA  
6151 CAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGT  
6201 CACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGA  
6251 CGCTGAGCAAAGCAGACTACGAGAAACACAAACTCTACGCCTGCGAAGTC  
6301 ACCCATCAGGGCCTGAGATCGCCCGTCAAAAGAGCTTCAACAAGGGGAG  
6351 AGTGTAGTTCTAGATAATTAATTAGGAGGAGATCTCGAGCTCGCGAAAG  
6401 CTTGGCACTGGCCGTCTGTTTTACAACGTCGTGACTGGGAAAACCCTGGCG  
6451 TTACCCAACTTAATCGCCTTGACGACATCCCCCTTTCGCCAGCCTCCTA  
6501 GGTGCACATCGATAAAATAAAAGATTTTTATTTAGTCTCCAGAAAAAGGGG  
6551 GGAATGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCC  
6601 ATTTTGAAGGCATGGAATAATACATAACTGAGAATAGAGAAGTTCAGAT  
6651 CAAGGTGAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCT  
6701 GTGGTAAGCAGTTCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGC  
6751 TGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTGCCCCGGCT  
6801 CAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTT  
6851 CTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACC  
6901 CTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCG  
6951 GCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGG  
7001 GGCGCCAGTCTCCCGATTGACTGAGTCGCGCGGGTACCCGTGTATCCAAT  
7051 AAACCTCTTGACGTTGCATCCGACTTGTGGTCTCGCTGTTCTTGGGAG  
7101 GGTCTCCTCTGAGTGATTGACTACCCGTGACGCGGGGTCTTTCATTTGGG  
7151 GGCTCGTCCGGGATCGGGAGACCCCTGCCAGGGACACCGACCCACCAC  
7201 CGGGAGGTAAGCTGGCTGCCTCGCGCGTTTCGGTGATGACGGTGAAGACC  
7251 TCTGACACATGCAGTCCCCGAGACGGTCACAGCTTGTCTGTAAGCGGAT  
7301 GCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGTG  
7351 TCGGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATACTG  
7401 GCTTAATATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGC  
7451 GGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGC  
7501 TCTTCCGCTTCTCTCGCTCACTGACTCGCTGCGCTCGGTCTGCGCTGCG  
7551 GCGAGCGGTATCAGTCACTCAAAGGCGGTAATACGGTTATCCACAGAAT  
7601 CAGGGGATAAACCGAGGAAAGAACATGTGAGCAAAGGCCAGCAAAGGCC  
7651 AGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC  
7701 CCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC  
7751 CGACAGGACTATAAAGATACCGGCGTTTCCCCCTGGAAGCTCCCTCGTG  
7801 CGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTCT  
7851 CCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCA  
7901 GTTCGGTGAGTTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCC  
7951 GTTCAGCCCGACCGCTGCGCCTTATCCGGTAACATATCGTCTTGAGTCCAA  
8001 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA  
8051 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGG  
8101 CCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCT  
8151 GAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAC  
8201 AAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACG  
8251 CGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC  
8301 TGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGAT  
8351 TATCAAAAAGGATCTTACCTAGATCCTTTTAAATTAAAAATGAAGTTTT  
8401 AAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATG  
8451 CTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCA  
8501 TAGTTGCCTGACTCCCCGTGCTGTAGATAACTACGATACGGGAGGGCTTA  
8551 CCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGC  
8601 TCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAA  
8651 GTGGTCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGG  
8701 GAAGCTAGAGTAAGTAGTTTCGCCAGTTAATAGTTTGCAGAACGTTGTTGC  
8751 CATTGCTGACGAGCATCGTGGTGTACGCTCGTCTGTTGGTATGGCTTCAT  
8801 TCAGTCCCGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTG  
8851 TGCAAAAAAGCGGTTAGTCTCTCGGTCTCCGATCGTTGTGAGAAGTAA  
8901 GTTGGCCGCGAGTGTATCACTCATGGTTATGGCAGCACTGCATAATTCTC  
8951 TTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCA  
9001 ACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCC  
9051 GCGGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAGTGC



Figure 17d

9101 TCATCATTGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCG  
9151 CTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTC  
9201 AGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGC  
9251 AAAATGCCGCAAAAAGGGAATAAGGGCGACACGAAATGTTGAATACTC  
9301 ATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCT  
9351 CATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGG  
9401 TTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATT  
9451 ATTATCATGACATTAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTTCG  
1. TCTTCAAGAAT

Features:

149-737 Moloney murine sarcoma virus 5' LTR  
807-1616 Extended Packaging Region  
1680-1735 EM7 promoter (bacteriophage T7 promoter)  
1754-2151 Blasticidin resistance gene coding sequence  
2310-2440 SV40 poly A signal and site  
2603-3420 CMV IE promoter  
3675-4988 G-protein-coupled receptor (GPCR)  
5071-5646 IRES  
5647-5703 Bovine a-lactalbumin signal peptide  
5704-6372 'humanized' antibody light chain  
6553-7146 MoMuLV 3' LTR  
7683Origin of replication  
9302-8442 b-Lactmase coding sequence

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